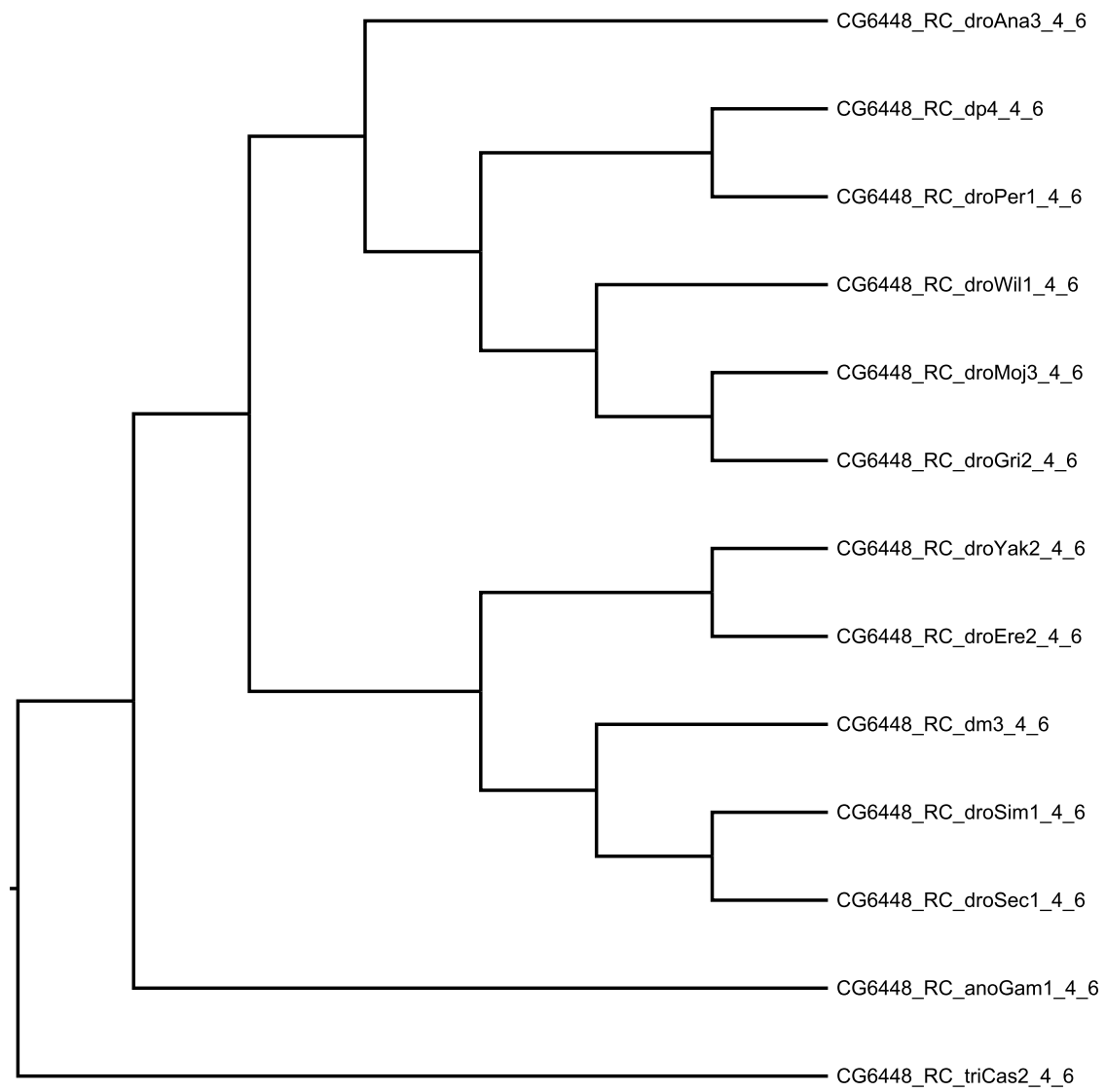
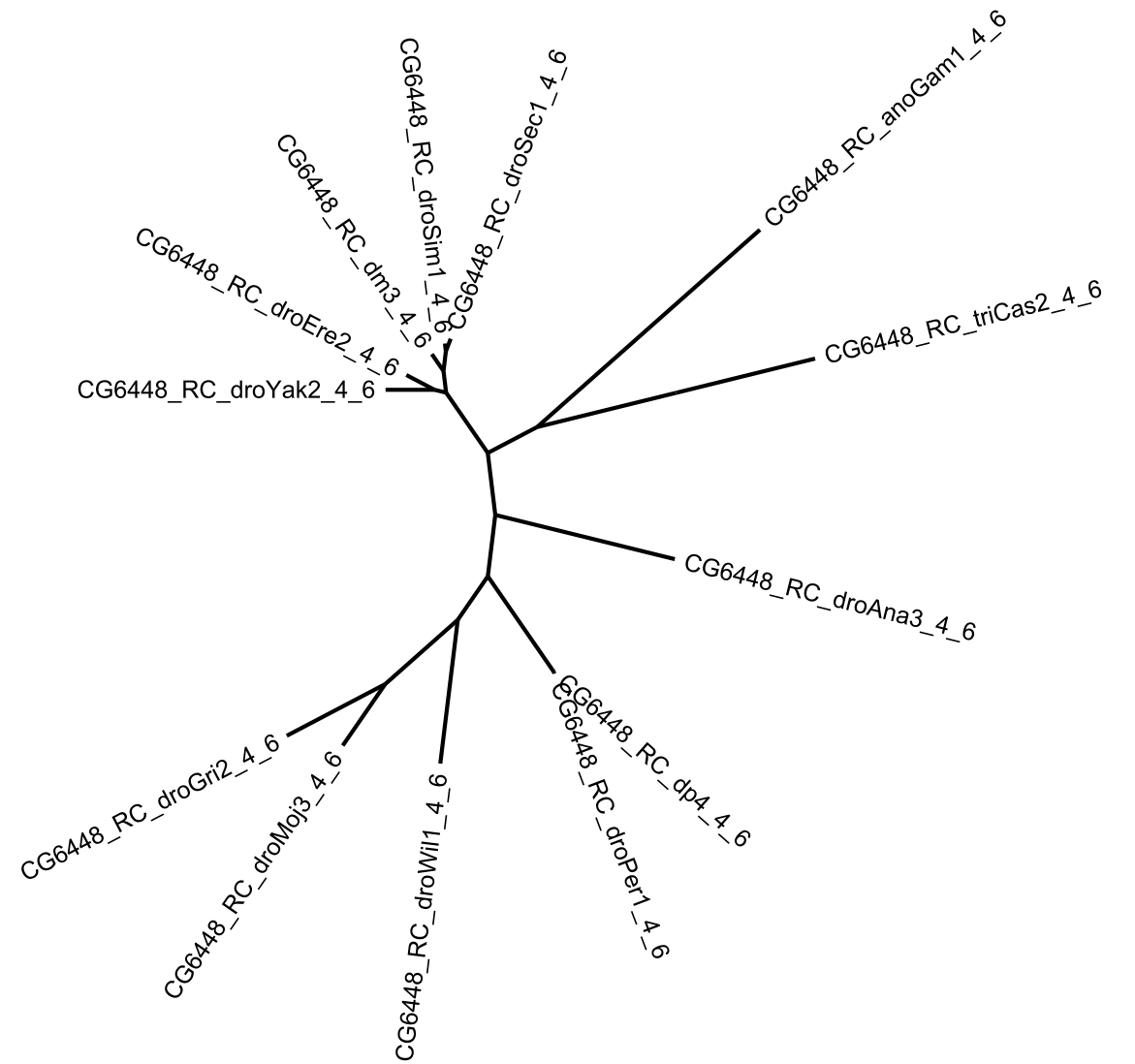


phylogeny = topology + branch lengths
branch lengths = rate x time
branch labels for support values
non-standard tip labels

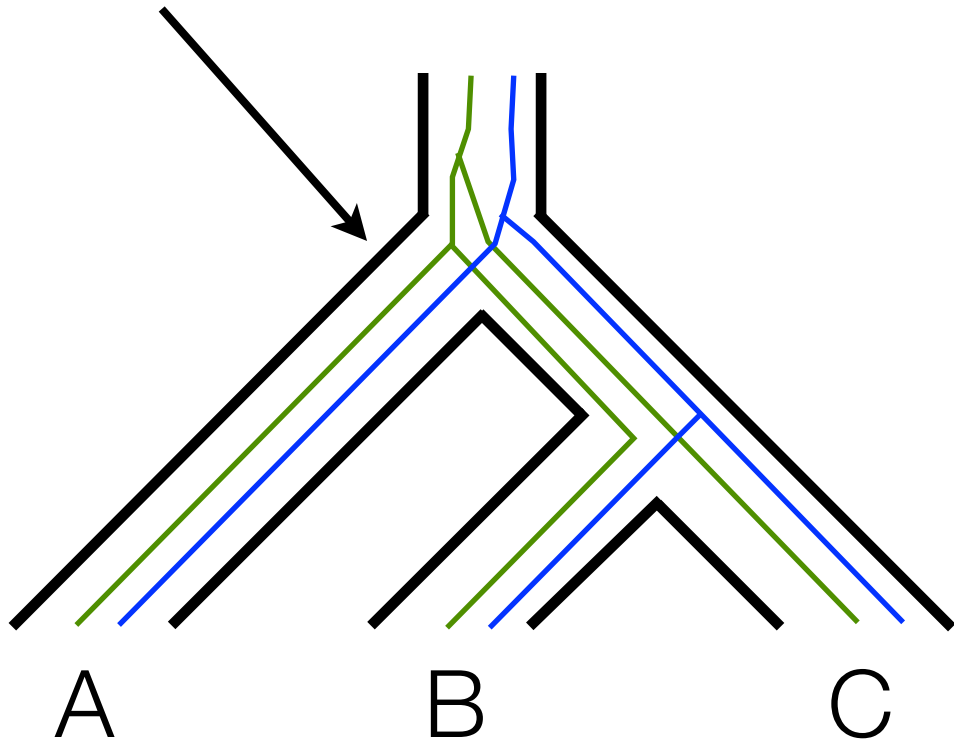


chronogram (rooted)

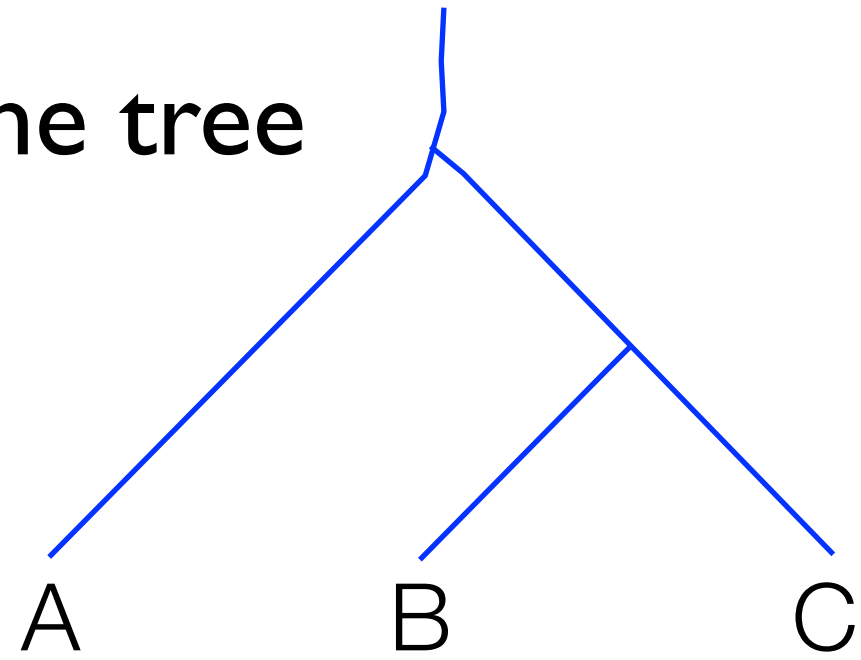


unrooted phylogeny

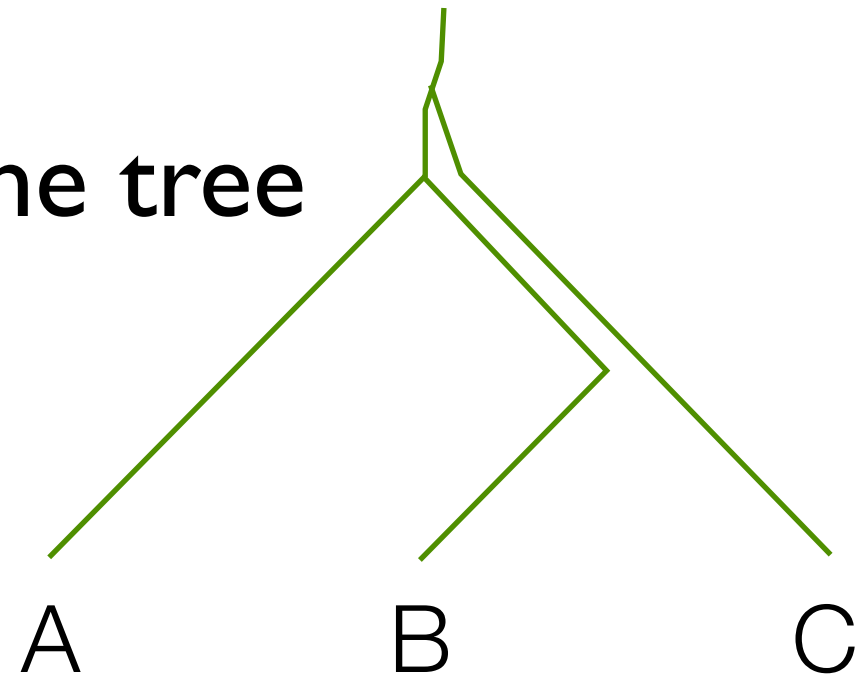
species tree



gene tree



gene tree



Input Data

- Molecular: DNA / RNA / protein
 - many genes; same or separate models
- Morphological (coded)
- Genome events: indels, gene order
- Many file formats!

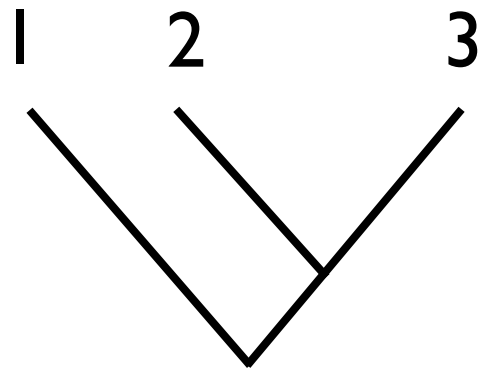
Alignment

ACCCTAATGGTTCATG		ACCCTAATGGTTCATG
ACCGTAATGTCAT		ACCGTAATG--TCAT-
ACGTATTGGTTCAT	→	A-CGTATTGGTTCAT-
AGCGTAAGGTTC		AGCGTAAGG-TTC---

Many methods / models

Know that sequences ARE aligned and HOW

Newick representation



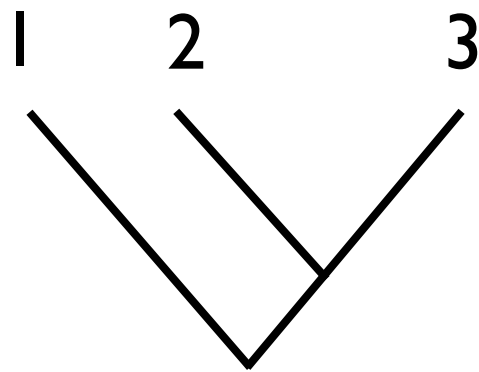
= ((1 , 2) , 3)

= (3 , (1 , 2))

= (1 , 2 , 3)

= [&U] ((1 , 2) , 3)

Newick representation



= ((1 , 2) , 3)

= (3 , (1 , 2))

= (1 , 2 , 3)

= [&U] ((1 , 2) , 3)

paml: ((1,2) #1, ((3,4) #2, 5), (6,7));

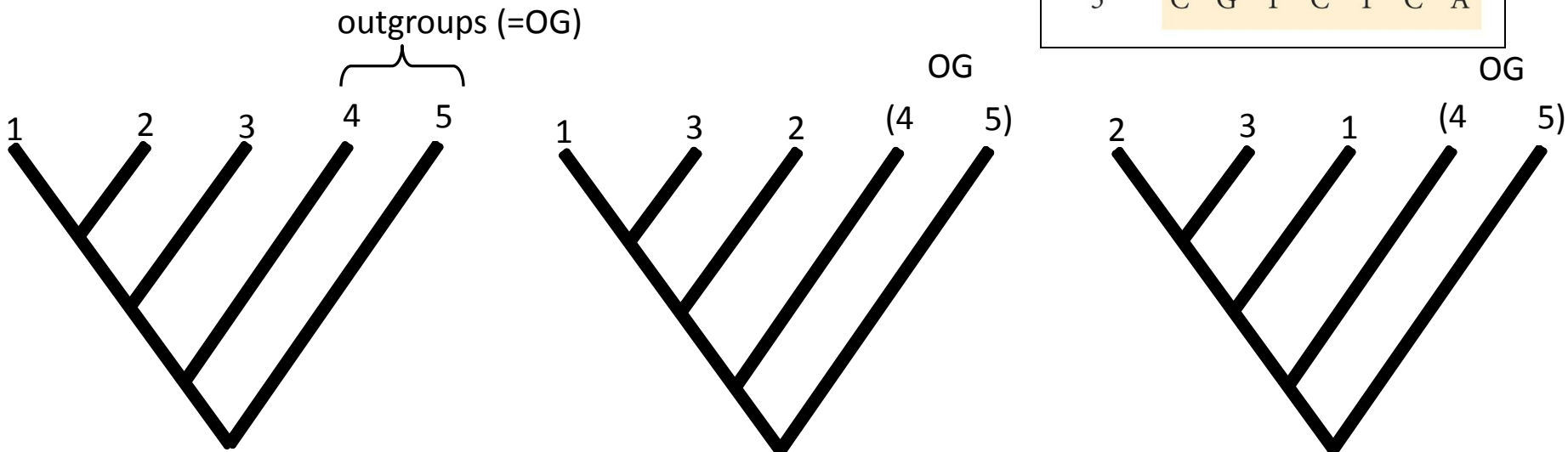
mrBayes: (1:0.06,2:0.03,(6:0.29,(7:0.33,8:1.21)0.71:0.14)0.99:0.26,(3:0.08,(4:0.06,5:0.12)0.98:0.02)0.99:0.04);

beast: (1[&rate_range={0.005999853264925051,0.15936238746770176},height_95%_HPD={0.0,3.552713678800501E-15},length_range={5.330803232139893,90.59447689989291},height_median=8.881784197001252E-16,length_95%_HPD={5.330803232139893,35.582740964218964},height=1.4122210685055808E-15,rate=0.06191554008174488,height_range={0.0,1.4210854715202004E-14},rate_median=0.05802603674557516,length=15.611001384387594,length_median=12.247276491265243,rate_95%_HPD={0.009705786691470234,0.12617823600055053}]:8.534139305707104,(((2[&rate_range={0.005701176008264525,0.12666823482278433},height_95%_HPD={0.0,3.552713678800501E-15},length_range...

Phylogenetic Reconstruction

- Parsimony → Cladogram ≠ Phylogram
- Maximum Likelihood = phylogram
- Bayesian Inference = phylogram

Species	Character						
	a	b	c	d	e	f	g
1	A	T	G	G	A	C	T
2	A	T	G	G	T	C	T
3	A	T	T	C	A	G	T
4	C	G	T	C	T	C	T
5	C	G	T	C	T	C	A



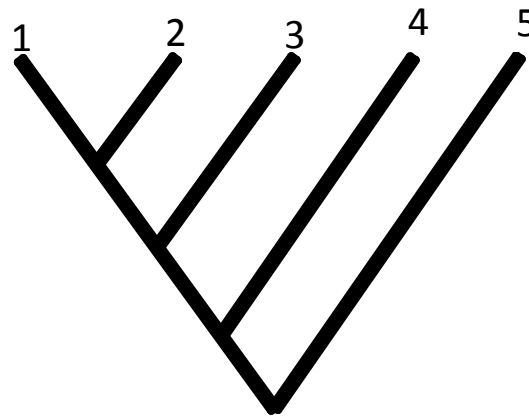
Maximum Likelihood and Bayesian Inference

- Both evaluated in terms of the likelihood of tree having come from the data
- Differ in the use of prior information and the exploration of parameter space
- Both typically use coalescent modeling and a Markov Chain Monte-Carlo process

Species	Character						
	a	b	c	d	e	f	g
1	A	T	G	G	A	C	T
2	A	T	G	G	T	C	T
3	A	T	T	C	A	G	T
4	C	G	T	C	T	C	T
5	C	G	T	C	T	C	A

Resulting trees and support

- Parsimony (Consistency Index and bootstrapping)
- ML (log-likelihood score and bootstrapping)
- BI (log-likelihood score, and posterior probabilities, and ESS scores from MCMC process)

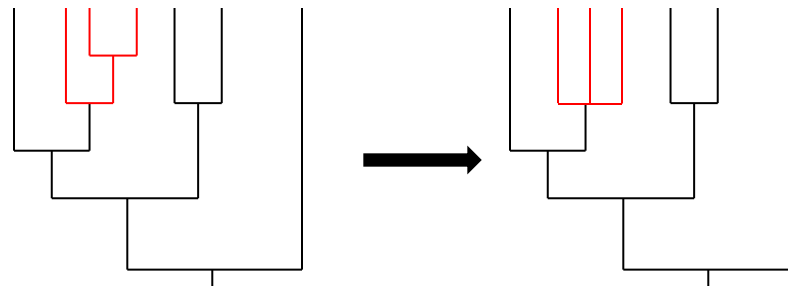


Species	Character						
	a	b	c	d	e	f	g
1	A	T	G	G	A	C	T
2	A	T	G	G	T	C	T
3	A	T	T	C	A	G	T
4	C	G	T	C	T	C	T
5	C	G	T	C	T	C	A

Consensus and ultrametric trees

- If there are several trees that are equally “precise”, then we have no way to differentiate between them, and sometimes the number of trees can be in the tens of thousands
- One common way to summarize these is to use a consensus tree, where poorly supported nodes (parts of the tree that differ among equally “likely” trees) are collapsed into a polytomy

Spp.	# trees
2	1
3	3
4	15
5	105
6	945
7	10,395
8	135,135
9	34,459,425
10	2.13E15
15	8.E21



Consensus and ultrametric trees

- How and which trees are summarized is rarely reported or repeatable
- Many analyses, such as time calibrated trees, depend on bifurcating trees (trees with no polytomies); typically researchers just choose one
- An ultrametric tree is one in which branch lengths represent time (aka a chronogram)
 - Not repeatable
 - Completely unreasonable to assign characteristics to a unit of analyses that may or may not exist

Divergence times

- For simple datasets, a tree imported from a previous analysis can be used
- BEAST allows for simultaneous estimation of a topology and calibrated nodes
 - No longer repeatable in the form of the template

Potential Reporting Standards

- Exact parameters and results of tree search algorithm
- What models were chosen and why
- What and how many parameters were estimated
- Complete list of equally likely trees